## SEQUENCE LISTING

- <110> DEROSE, Richard
   CHAUBET, Nicole
   GIGOT, Claude (deceased)
- <120> ISOLATED DNA SEQUENCE CAPABLE OF SERVING AS REGULATORY ELEMENT IN A CHIMERIC GENE WHICH CAN BE USED FOR THE TRANSFORMATION OF PLANTS
- <130> 022650-453
- <140> 09/000,062
- <141> 1998-05-29
- <150> PCT/FR96/01109
- <151> 1996-07-17
- <150> FR 95/08980
- <151> 1995-07-19
- <160> 22
- <170> PatentIn Ver. 2.0
- <210> 1
- <211> 1713
- <212> DNA
- <213> Zea mays

<400> 1

aatcaattte acacaggaaa cagetatgae catgattaeg aattegggee egggeggtg 60
atceggegge ggcageggeg geggeggtge aggegggtge egaggagate gtgetgeage 120
ccatcaagga gatctgggge agegteaage tgceggggte caagtegett tecaacegga 180
teeteetaet egeegeettg teegagggga caacagtggt tgataacetg etgaacagtg 240
aggatgteea etacatgete ggggeettga ggactettgg tetetetgte gaageggaca 300
aaggteecaa aagagetgta ettgttgget etggtggaaa gtteecagtt gaggatgeta 360
aagaggaagt geagetette ttgggggaatg etggaactge aatgeggeea ttgacageg 420
etgttaetge tgetggtgga aatgeaactt aegtgettga tggagtaeca agaatgaggg 480
aggacecat tggegaettg gttgteggat tgaageaget tggtgeagat gttgattgtt 540
teettggeae tgactgeea egtgttegtg teaatggaat eggagggeta eetggtggea 600
aggteaaget gtetggetee ateageagte agtaettgag tgeettgetg atggetgete 660
etttggetet tggggatgtg gagattgaaa teattgataa attaatetee atteegtaeg 720

tcgaaatgac attgagattg atggaccgtt ttggtgtgaa agcagagcat tctgatagct 780 gggacagatt ctacattaag ggaggtcaaa aatacaagtc ccctaaaaat gcctatgttg 840 aaggtgatgc ctcaagcgca agctatttct tggctggtgc tgcaattact ggagggactg 900 tgactgtgga aggttgtggc accaccagtt tgcagggtga tgtgaagttt gctgaggtac 960 tggagatgat gggagcgaag gttacatgga ccgagactag cgtaactgtt actccccac 1020 cgcgggagcc atttgggagg aaacacctca aggcgattga tgtcaacatc aacaagatgc 1080 etgatgtege catgactett getgtggttg ceetetttge egatggeeeg acagecatea 1140 gagacgtggc ttcctggaga gtaaaggaga ccgagaggat ggttgcgatc cggacggagc 1200 taaccaaget gggagcatet gttgaggaag ggeeggaeta etgeateate aegeegeegg 1260 agaagetgaa egtgaeggeg ategaeaegt aegaegaeea eaggatggee atggeettet 1320 cccttgccgc ctgtgccgag gtccccgtca ccatccggga ccctgggtgc acccggaaga 1380 ccttccccga ctacttcgat gtgctgagca ctttcgtcaa gaattaataa agcgtgcgat 1440 actaccacgc agcttgattg aagtgatagg cttgtgctga ggaaatacat ttcttttgtt 1500 ctgtttttct ctttcacggg attaagtttt gagtctgtaa cgttagttgt ttgtagcaag 1560 aaaaaaaaa aaaaaaaaa aacccgggaa ttc 1713

```
<210> 2
<211> 1340
<212> DNA
<213> Zea mays
<220>
<221> CDS
<222> (6)..(1337)
```

<400> 2

ccatg gcc ggc gcc gag gag atc gtg ctg cag ccc atc aag gag atc tcc 50
Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser

ggc acc gtc aag ctg ccg ggg tcc aag tcg ctt tcc aac cgg atc ctc 98 Gly Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu 20 25 30

cta ctc gcc gcc ctg tcc gag ggg aca aca gtg gtt gat aac ctg ctg 146 Leu Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu 35 40 45

aac · Asn					cac His											194
				_	gac Asp		-	_		_	_	-	_	_		242
					cca Pro 85											290
					gga Gly											338
					aat Asn										_	386
_					att Ile		_	_	_	-			_	_		434
					tgt Cys											482
					999 Gly 165			_								530
					tac Tyr											578
	Leu		Asp	Val	gag Glu	Ile		Ile	Ile	qaA	Lys	Leu		Ser		626
					aca Thr											674
					agc Ser		_									722
					aaa Lys 245		-		-							770
gca	agc	tat	ttc	ttg	gct	ggt	gct	gca	att	act	gga	<b>3</b> 33	act	gtg	act	818

Ala	Ser	Tyr	Phe	Leu 260	Ala	Gly	Ala	Ala	Ile 265	Thr	Gly	Gly	Thr	Val 270	Thr	
		ggt Gly														866
		ctg Leu 290														914
		gtt Val														962
		att Ile														1010
		gtg Val														1058
		tcc Ser														1106
		cta Leu 370														1154
		atc Ile														1202
		gac Asp			_	_	_	_				_	_	_	_	1250
		ccc Pro														1298
		tac Tyr											taa			1340

<210> 3

<211> 444

<212> PRT

<213> Zea mays

<400> 3

Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly

£

ļ.

Find Con

ļ.i

Thr	Val	Lys	Leu	Pro	Gly	Ser	Lys	Ser	Leu	Ser	Asn	Arg	Ile	Leu	Leu
			20					25					30		

Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn 35 40 45

Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu 50 60

Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Gly Cys
65 70 75 80

Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe 85 90 95

Leu Gly Asn Ala Gly Thr Ala Met Arg Pro Leu Thr Ala Ala Val Thr
100 105 110

Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met 115 120 125

Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
130 135 140

Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val 145 150 155 160

Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser 165 170 175

Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala 180 185 190

Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro 195 200 205

Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala 210 215 220

Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gln Lys 225 230 235 240

Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala 245 250 255

Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val 260 265 270

Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu 275 280 285

Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val 290 295 300

Thr 305	Val	Thr	Gly	Pro	Pro 310	Arg	Glu	Pro	Phe	Gly 315	Arg	Lys	His	Leu	Lys 320	
Ala	Tle	Asp	Val	Asn 325	Met	Asn	Lys	Met	Pro 330	Asp	Val	Ala	Met	Thr 335	Leu	
Ala	Val	Val	Ala 340	Leu	Phe	Ala	Asp	Gly 345	Pro	Thr	Ala	Ile	Arg 350	Asp	Val	
Ala	Ser	Trp 355	Arg	Val	Lys	Glu	Thr 360	Glu	Arg	Met	Val	Ala 365	Ile	Arg	Thr	
Glu	Leu 370	Thr	Lys	Leu	Gly	Ala 375	Ser	Val	Glu	Glu	Gly 380	Pro	Asp	Tyr	Cys	
Ile 385	Ile	Thr	Pro	Pro	Glu 390	Lys	Leu	Asn	Val	Thr 395	Ala	Ile	Asp	Thr	Tyr 400	
Asp	Asp	His	Arg	Met 405	Ala	Met	Ala	Phe	Ser 410	Leu	Ala	Ala	Cys	Ala 415	Glu	
Val	Pro	Val	Thr 420	·Ile	Arg	Asp	Pro	Gly 425	Cys	Thr	Arg	Lys	Thr 430	Phe	Pro	
Asp	Tyr	Phe 435	Asp	Val	Leu	Ser	Thr 440	Phe	Val	Lys	Asn					
<213	0> 4 1> 13 2> Di 3> Ze	A	ays												·	
	0> 1> CI 2> (6		(133	7)												
										ln Pi					to too le Ser 15	50
				ctg Leu 20												98
cta Leu	ctc Leu	gcc Ala	gcc Ala 35	ctg Leu	tcc Ser	gag Glu	Gly aaa	aca Thr 40	aca Thr	gtg Val	gtt Val	gat Asp	aac Asn 45	ctg Leu	ctg Leu	146
				gtc Val												194
ctc	tct	gtc	gaa	gcg	gac	aaa	gct	gcc	aaa	aga	gct	gta	gtt	gtt	ggc	242

Leu	Ser 65	Val	Glu	Ala	Asp	Lys 70	Ala	Ala	Lys	Arg	Ala 75	Val	Val	Val	Gly	
	ggt Gly															290
	ttg Leu															338
	gct Ala															386
_	agg Arg					Gly	_	_	_							434
	gca Ala 145															482
	aat Asn															530
	atc Ile															578
	ctt Leu															626
	tac Tyr															674
	gag Glu 225															722
	tac Tyr															770
	agc Ser															818
gtg Val	gaa Glu	ggt Gly	tgt Cys 275	ggc	acc Thr	acc Thr	agt Ser	ttg Leu 280	cag Gln	ggt Gly	gat Asp	gtg Val	aag Lys 285	ttt Phe	gct Ala	866

	gta Val															914
	act Thr 305															962
	gcg Ala															1010
	gct Ala		_	_			_	_		_				-	-	1058
	gct Ala															1106
	gag Glu															1154
	atc Ile 385															1202
tac Tyr 400	gac Asp	gac Asp	cac His	agg Arg	atg Met 405	gcg Ala	atg Met	gcc Ala	ttc Phe	tcc Ser 410	ctt Leu	gcc Ala	gcc Ala	tgt Cys	gcc Ala 415	1250
	gtc Val															1298
	gac Asp												taa			1340

<210> 5

<211> 444

<212> PRT

<213> Zea mays

<400> 5

Ala Gly Ala Glu Glu Ile Val Leu Gln Pro Ile Lys Glu Ile Ser Gly
1 5 10 15

Thr Val Lys Leu Pro Gly Ser Lys Ser Leu Ser Asn Arg Ile Leu Leu 20 25 30

Leu Ala Ala Leu Ser Glu Gly Thr Thr Val Val Asp Asn Leu Leu Asn 35 40 45

- Ser Glu Asp Val His Tyr Met Leu Gly Ala Leu Arg Thr Leu Gly Leu 50 55 60
- Ser Val Glu Ala Asp Lys Ala Ala Lys Arg Ala Val Val Gly Cys
  65 70 75 80
- Gly Gly Lys Phe Pro Val Glu Asp Ala Lys Glu Glu Val Gln Leu Phe 85 90 95
- Leu Gly Asn Ala Gly Ile Ala Met Arg Ser Leu Thr Ala Ala Val Thr
  100 105 110
- Ala Ala Gly Gly Asn Ala Thr Tyr Val Leu Asp Gly Val Pro Arg Met
  115 120 125
- Arg Glu Arg Pro Ile Gly Asp Leu Val Val Gly Leu Lys Gln Leu Gly
  130 135 140
- Ala Asp Val Asp Cys Phe Leu Gly Thr Asp Cys Pro Pro Val Arg Val 145 150 155 160
- Asn Gly Ile Gly Gly Leu Pro Gly Gly Lys Val Lys Leu Ser Gly Ser 165 170 175
- Ile Ser Ser Gln Tyr Leu Ser Ala Leu Leu Met Ala Ala Pro Leu Ala 180 185 190
- Leu Gly Asp Val Glu Ile Glu Ile Ile Asp Lys Leu Ile Ser Ile Pro 195 200 205
- Tyr Val Glu Met Thr Leu Arg Leu Met Glu Arg Phe Gly Val Lys Ala 210 215 220
- Glu His Ser Asp Ser Trp Asp Arg Phe Tyr Ile Lys Gly Gln Lys 225 230 235 240
- Tyr Lys Ser Pro Lys Asn Ala Tyr Val Glu Gly Asp Ala Ser Ser Ala 245 250 255
- Ser Tyr Phe Leu Ala Gly Ala Ala Ile Thr Gly Gly Thr Val Thr Val 260 265 270
- Glu Gly Cys Gly Thr Thr Ser Leu Gln Gly Asp Val Lys Phe Ala Glu 275 280 285
- Val Leu Glu Met Met Gly Ala Lys Val Thr Trp Thr Glu Thr Ser Val 290 295 300
- Thr Val Thr Gly Pro Pro Arg Glu Pro Phe Gly Arg Lys His Leu Lys 305 310 315 320
- Ala Ile Asp Val Asn Met Asn Lys Met Pro Asp Val Ala Met Thr Leu 325 330 335
- Ala Val Val Ala Leu Phe Ala Asp Gly Pro Thr Ala Ile Arg Asp Val

T.

 340 345 350

Ala Ser Trp Arg Val Lys Glu Thr Glu Arg Met Val Ala Ile Arg Thr 355 360 365

Glu Leu Thr Lys Leu Gly Ala Ser Val Glu Glu Gly Pro Asp Tyr Cys 370 375 380

Ile Ile Thr Pro Pro Glu Lys Leu Asn Val Thr Ala Ile Asp Thr Tyr 385 390 395 400

Asp Asp His Arg Met Ala Met Ala Phe Ser Leu Ala Ala Cys Ala Glu 405 410 415

Val Pro Val Thr Ile Arg Asp Pro Gly Cys Thr Arg Lys Thr Phe Pro 420 425 430

Asp Tyr Phe Asp Val Leu Ser Thr Phe Val Lys Asn 435 440

<210> 6

<211> 418

<212> DNA

<213> Zea mays

<400> 6

tgaggtacga ttettegate etettgatt tteetggaaa tatttttee gtgategtae 60

aactactgga ategetegat aggtggtacg aaattaggeg agattagttt etattettgg 120

ccattatett gtttettege egaatgatet teegtataaa gattttaggt tagagatgaa 180

tegtataget agattteate accagatagt ttetttgtet agaatetetg aaattetega 240

tagtttteae atgtgtaaat agattgtet tatteggega ttgttgatta gggttttgat 300

tttettgatt atgegattge aattagggat tttetttggt tttgtgttga teetaegata 360

catteetgea attgaataeg tatggateta aatettgtta atttgttgaa eagateee 418

<210> 7

<211> 494

<212> DNA

<213> Zea mays

400> 7

ctcaggcgaa gaacaggtat gatttgtttg taattagatc aggggtttag gtctttccat 60 tactttttaa tgtttttct gttactgtct ccgcgatctg attttacgac aatagagttt 120 cgggttttgt cccattccag tttgaaaata aacgtccgtc ttttaagttt gctggatcga 180 taaacctgtg aagattgagt ctagtcgatt tattggatga tccattcttc atcgttttt 240

tettgetteg a	aagttctgta	taaccagatt	tgtctgtgtg	cgattgtcat	tacctagccg	300
tgtatcgaga a	actagggttt	tcgagtcaat	tttgcccctt	ttggttatat	ctggttcgat	360
aacgattcat o	ctggattagg	gttttaagtg	gtgacgttta	gtattccaat	ttcttcaaaa	420
tttagttatg g	gataatgaaa	atcccgaatt	gactgttcaa	tttcttgtta	aatgcgcaga	480
tecegggate t	tgcg					494
<210> 8						
<211> 20						
<212> DNA <213> Zea ma	ave					
\213\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	.ys					
<400> 8 gctctgctca t	ratataataa					
geretgetea t	-greigeree					20
<210> 9						
<210> 9						
<212> DNA						
<213> Zea ma	ıys					
<400> 9						
geeegeeett g	gacaaagaaa					20
<210> 10						
<211> 10						
<212> DNA						
<213> Zea ma	ıys					
<400> 10						
aattcccggg						10
<210> 11						
<211> 38			•			
<212> DNA <213> Zea ma	vs					
	1-					
<400> 11						
aattaagctc t	ayayteyae (	ctgcaggcat	gcaagctt			38
<210> 12 <211> 41						
<212> DNA						
<213> Zea ma	ys					
<400> 12						
gageegaget e	catggccgg (	caccasaas	atcatactac a	<b>a</b>		41

<210> 13	
<211> 37	
<212> DNA	
<213> Zea mays	
<400> 13	
gcacgatete eteggegeeg gecatggage teggete	37
	3,
<210> 14	
<211> 25	
<212> DNA	
<213> Zea mays	
•	
<400> 14	
ccacaggatg gcgatggcct totec	25
	23
<210> 15	
<211> 33	
<212> DNA	
<213> Zea mays	
,	
<400> 15	•
gaatgotgga atogoaatgo ggocattgao ago	22
gaacgeegga acogeaacge ggeeactgae age	33
<210> 16	
<211> 33	
<212> DNA	
<213> Zea mays	
12137 200 may 5	
<400> 16	
gaatgetgga actgcaatge ggteettgae age	33
gaacgeegga acegeaacge ggeeeetgae age	33
<210> 17	
<211> 34	
<211> 34 <212> DNA	
<213> Zea mays	
<400> 17	
cttggggaat gctgccatcg caatgcggcc attg	34
<210> 18	
<211> 36	
<212> DNA	
<213> Zea mays	
.400- 10	
<400> 18	
ggggaatget ggaategeaa tgeggteett gacage	36
1	
<210> 19	

<211> 20 <212> DNA	
<213> Zea mays	
<400> 19 ;	
taatttgttg aacagatccc	20
<210> 20	
<211> 18	
<211> 16	
<213> Zea mays	
<400> 20	
taaacaactt gtctaggg	18
<210> 21	
<211> 18	
<212> DNA	
<213> Zea mays	
<400> 21	
cagatcccgg gatctgcg	18
-	
<210> 22	
<211> 20	•
<212> DNA	
<213> Zea mays	
<400> 22	
gcgtctaggg ccctagacgc	20